Modelling eradication potential of a newly developed gene drive strategy in mice using spatially explicit agent-based simulations

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Abstract: Invasive rodents are a major cause of environmental damage, biodiversity loss and loss of agricultural productivity (Paini et al. 2016, Godwin et al. 2019). Unlike insects, genetic biocontrol strategies including population suppressing gene drives with biased inheritance have not been developed in rodents. In this talk, we will introduce a newly developed gene drive strategy (t_{CRISPR}) that will leverage the naturally occurring male meiotic drive element in mice (*t* haplotype) with Cas9 and a gRNA that will cleave and create loss-of-function (LOF) alleles in the male germ line of a female fertility gene (Gierus et al. 2022). Using large-scale spatially explicit individual-based model, we show that t_{CRISP} can eradicate island populations under a range of realistic field-based parameter values (Figure 1).

We also demonstrate proof of concept for eradication potential of a classic homing drive in rats in light of recent empirical data. Lastly, we discuss the scalability of gene drives for other vertebrate pest eradications (Birand et al. 2022).
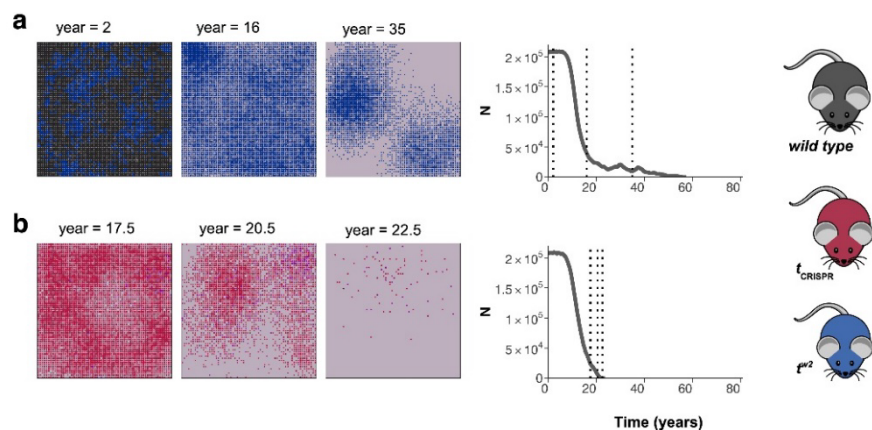
Figure 1. Sample simulations using two strategies, namely, t_{CRISPR} and t^{w2} (and resistant genotypes, Prl*). Shown in order are three snapshots of the spatial distribution of mouse populations, total population size, and the allele frequency change through time, starting with the inoculation of t haplotype individuals at year = 0 (dashed lines in the plots correspond to the years of the snapshots)

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